Remarks/Arguments:

Applicants wish to thank Primary Examiner Patricia Ann Duffy for expressly indicating withdrawal of the rejections against—and allowance of—claims 27-30 (previously presented). Applicants also wish to thank Primary Examiner Duffy for expressly indicating withdrawal of the rejections under §112, 2nd ¶, §102(b), and §103(a) against claims 20-25.

Claims 20, 21, 24, 25, and 27-30 are pending, with claims 27-30 standing allowed, as indicated above.

Claims 20, 21, and 25 are currently amended.

Claims 1-19, 22, 23, 26, and 31-60 are cancelled, without prejudice or disclaimer.

Claim 21 is amended to correct a clerical error.

Claim 20 is amended, hereby, with respect to the recited Markush group alternatives "fragment of SEQ ID NO: 2" and "derived sequence of SEQ ID NO: 2." More precisely, claim 20 is amended (i) by changing the minimum number of "consecutive nucleotides"—in each of the recited "fragment" and "derived sequence"—from "14" to "30" and (ii) by adding the *proviso* "excluding a nucleotide chain of at least 30 nucleotides within or overlapping the region defined by nucleotides 237-270 of SEQ ID NO: 2." The region of SEQ ID NO:2 constituting nucleotides 237-570 is described in the present specification (page 20, lines 3-8) as a region exhibiting 68% homology with a virK gene encoding a virulence protein of *Shigella flexneri*. Accordingly, one skilled in the art would readily find that the present specification inferentially teaches a preference for fragments and sequences outside the region 237-570 of SEQ ID NO:2, i.e., in order to detect

enterohaemorrhagic *E. Coli* (EHECs), fragments or sequences outside the region 237-570 of SEQ ID NO:2 are preferred since the region 237-570 shows some homology with sequences found in a microorganism different from an enterohaemorrhagic *E. Coli*.

Claim 25 is amended by being rewritten as an independent claim.

Claims 20 and 21 remain rejected under 35 USC 112, first paragraph, as allegedly failing to comply with the written description requirement. Reconsideration is requested in view of the changes to the rejected claims effected hereby, taken in conjunction with the following remarks.

Amended claim 20 is limited to the "fragment" and "derived sequence" of SEQ ID NO:2 comprising a nucleotide chain of at least 30 (instead of 14) consecutive nucleotides, excluding a chain within or overlapping the region defined by nucleotides 237 to 570 of SEQ ID NO:2.

A search in databases for sequences producing significant alignment with SEQ ID NO:2 did not enable to identify any sequence comprising at least 30 consecutive nucleotides of SEQ ID NO:2, outside of the region 237-570 of SEQ ID NO:2, except the p)157 plasmid (see the result of sequence alignments herewith).

Sequences from *Photorhabdus luminescens* (EMBL:Bx571861.1) and *Bacteroids thetaiotaomicron* (Genbank: AEO15928.1) show 100% local identity with SEQ ID NO:2 but only on a stretch of 24 nucleotides and 23 nucleotides, respectively.

Therefore, present claim 20 defines the structural features which determine the function of recognizing an EHEC.

With respect to present, rejected claim 21—and the recited Markush group alternative "sequence derived from SEQ ID NO:1"—the claim 21 language, itself, makes it clear that the recited "sequence derived from SEQ ID NO:1" must include at least 14 consecutive nucleotides of SEQ ID NO:1, which at least 14 consecutive nucleotides must contain nucleotides 400 to 407.

Thus, the critical nucleotides for the recognition of *E. Coli* O157:H7 are identified in claim 21 as nucleotides 400-407 of SEQ ID NO:1.

Indeed, applicant performed a search (copy attached, hereto) in the databases Genbank, EMBL, DDBJ and PDB for sequences from *E. Coli* matching SEQ ID NO:1. It was found that the only *E. Coli* strain containing a sequence of 14 consecutive nucleotides of SEQ ID NO:1, including nucleotides 400-407, is *E. Coli* O157:H7.

Sequences from other *E. Coli* strains or microorganisms (such as *Shigelli flexneri*) matching with a portion of SEQ ID NO:1 correspond either to parts of katP or IS91 gene. Accordingly, the specific detection of a IS91-katP junction by hybridization with a nucleic acid and containing a sequence of 14 consecutive nucleotides of SEQ ID NO:1, including nucleotides 400-407 of SEQ ID NO:1, or its complement, enables specific detection of *E. Coli* O157:H7.

Furthermore, the definition of the sequence derived from SEQ ID NO:1 ensures that the derived sequence will be complementary to at least a stretch of 14 consecutive nucleotides that includes nucleotides 400-407 of SEQ ID NO:1, or its complementary sequence. Variability can be tolerated outside of this stretch of 14 nucleotides without affecting its capacity to hybridize

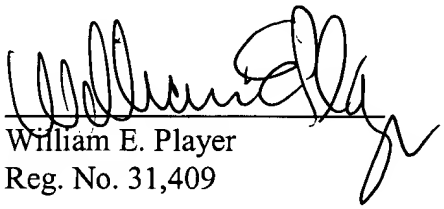
specifically to the region 400-407 of SEQ ID NO:1 or its complementary sequence, thereby enabling for detecting *E. Coli* O157:H7.

For the foregoing reasons, the rejection under §112, 1st ¶, of claims 20 and 21—and the objection to claims24 and 25 for being dependent, respectively, thereon—are overcome. Withdrawal of the rejection and objection appear to be in order.

Favorable action is requested.

Respectfully submitted,

JACOBSON HOLMAN PLLC

By 
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